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RAW SEQUENCE LISTING

DATE: 06/27/2002

PATENT APPLICATION: US/08/813,323B

TIME: 13:04:49

Input Set : A:\50659.txt

Output Set: N:\CRF3\06272002\H813323B.raw

3 <110> APPLICANT: Baltimore, David
 4 Cheng, Genhong
 5 Ye, Zheng-Sheng
 6 Lederman, Seth
 7 Cleary, Aileen
 9 <120> TITLE OF INVENTION: Truncated Craf-1 Inhibits CD40 Signalling
 11 <130> FILE REFERENCE: 0575/50659
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/08/813,323B
 C--> 14 <141> CURRENT FILING DATE: 2002-06-17
 16 <160> NUMBER OF SEQ ID NOS: 5
 18 <170> SOFTWARE: PatentIn version 3.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 567
 22 <212> TYPE: PRT
 23 <213> ORGANISM: Mouse Sp.
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 32 20 25 30
 35 Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu Asp
 36 35 40 45
 39 Lys Tyr Lys Cys Glu Lys Cys Arg Leu Val Leu Cys Asn Pro Lys Gln
 40 50 55 60
 43 Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu Leu
 44 65 70 75 80
 47 Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Ile Lys
 48 85 90 95
 51 Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala Leu
 52 100 105 110
 55 Gln Val Tyr Cys Arg Asn Glu Gly Arg Gly Cys Ala Glu Gln Leu Thr
 56 115 120 125
 59 Leu Gly His Leu Leu Val His Leu Lys Asn Glu Cys Gln Phe Glu Glu
 60 130 135 140
 63 Leu Pro Cys Leu Arg Ala Asp Cys Lys Glu Lys Val Leu Arg Lys Asp
 64 145 150 155 160
 67 Leu Arg Asp His Val Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr Cys
 68 165 170 175
 71 Ser His Cys Lys Ser Gln Val Pro Met Ile Lys Leu Gln Lys His Glu
 72 180 185 190
 75 Asp Thr Asp Cys Pro Cys Val Val Val Ser Cys Pro His Lys Cys Ser
 76 195 200 205
 79 Val Gln Thr Leu Leu Arg Ser Glu Leu Ser Ala His Leu Ser Glu Cys

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83 Val Asn Ala Pro Ser Thr Cys Ser Phe Lys Arg Tyr Gly Cys Val Phe
84 225      230      235      240
87 Gln Gly Thr Asn Gln Gln Ile Lys Ala His Glu Ala Ser Ser Ala Val
88      245      250      255
91 Gln His Val Asn Leu Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys Lys
92      260      265      270
95 Val Ser Leu Leu Gln Asn Glu Ser Val Glu Lys Asn Lys Ser Ile Gln
96      275      280      285
99 Ser Leu His Asn Gln Ile Cys Ser Phe Glu Ile Glu Ile Glu Arg Gln
100      290      295      300
103 Lys Glu Met Leu Arg Asn Asn Glu Ser Lys Ile Leu His Leu Gln Arg
104 305      310      315      320
107 Val Ile Asp Ser Gln Ala Glu Lys Leu Lys Glu Leu Asp Lys Glu Ile
108      325      330      335
111 Arg Pro Phe Arg Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser Ser
112      340      345      350
115 Val Glu Ser Leu Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp Lys
116      355      360      365
119 Ser Ala Gly Gln Ala Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln Leu
120      370      375      380
123 Ser Arg His Asp Gln Thr Leu Ser Val His Asp Ile Arg Leu Ala Asp
124 385      390      395      400
127 Met Asp Leu Arg Phe Gln Val Leu Glu Thr Ala Ser Tyr Asn Gly Val
128      405      410      415
131 Leu Ile Trp Lys Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala Val
132      420      425      430
135 Met Gly Lys Thr Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly Tyr
136      435      440      445
139 Phe Gly Tyr Lys Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly Met
140      450      455      460
143 Gly Lys Gly Thr His Leu Ser Leu Phe Phe Val Ile Met Arg Gly Glu
144 465      470      475      480
147 Tyr Asp Ala Leu Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu Met
148      485      490      495
151 Leu Met Asp Gln Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe Lys
152      500      505      510
155 Pro Asp Pro Asn Ser Ser Ser Phe Lys Lys Pro Thr Gly Glu Met Asn
156      515      520      525
159 Ile Ala Ser Gly Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu Asn
160      530      535      540
163 Gly Thr Tyr Ile Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val Asp
164 545      550      555      560
167 Thr Ser Asp Leu Pro Asp Pro
168      565
171 <210> SEQ ID NO: 2
172 <211> LENGTH: 568
173 <212> TYPE: PRT
174 <213> ORGANISM: Homo Sapiens

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176 <400> SEQUENCE: 2

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183          20          25          30
186 Val Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu
187          35          40          45
190 Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys
191          50          55          60
194 Gln Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu
195 65          70          75          80
198 Leu Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val
199          85          90          95
202 Lys Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala
203          100          105          110
206 Leu Gln Ile Tyr Cys Arg Asn Glu Ser Arg Gly Cys Ala Glu Gln Leu
207          115          120          125
210 Thr Leu Gly His Leu Leu Val His Leu Lys Asn Asp Cys His Phe Glu
211          130          135          140
214 Glu Leu Pro Cys Val Arg Pro Asp Cys Lys Glu Lys Val Leu Arg Lys
215 145          150          155          160
218 Asp Leu Arg Asp His Val Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr
219          165          170          175
222 Cys Ser His Cys Lys Ser Gln Val Pro Met Ile Ala Leu Gln Lys His
223          180          185          190
226 Glu Asp Thr Asp Cys Pro Cys Val Val Val Ser Cys Pro His Lys Cys
227          195          200          205
230 Ser Val Gln Thr Leu Leu Arg Ser Glu Leu Ser Ala His Leu Ser Glu
231          210          215          220
234 Cys Val Asn Ala Pro Ser Thr Cys Ser Phe Lys Arg Tyr Gly Cys Val
235 225          230          235          240
238 Phe Gln Gly Thr Asn Gln Gln Ile Lys Ala His Glu Ala Ser Ser Ala
239          245          250          255
242 Val Gln His Val Asn Leu Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys
243          260          265          270
246 Lys Val Ser Leu Leu Gln Asn Glu Ser Val Glu Lys Asn Lys Ser Ile
247          275          280          285
250 Gln Ser Leu His Asn Gln Ile Cys Ser Phe Glu Ile Glu Ile Glu Arg
251          290          295          300
254 Gln Lys Glu Met Leu Arg Asn Asn Glu Ser Lys Ile Leu His Leu Gln
255 305          310          315          320
258 Arg Val Ile Asp Ser Gln Ala Glu Lys Leu Lys Glu Leu Asp Lys Glu
259          325          330          335
262 Ile Arg Pro Phe Arg Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser
263          340          345          350
266 Ser Val Glu Ser Leu Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp
267          355          360          365
270 Lys Ser Ala Gly Gln Val Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln
271          370          375          380

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274 Leu Ser Arg His Asp Gln Met Leu Ser Val His Asp Ile Arg Leu Ala
 275 385 390 395 400
 278 Asp Met Asp Leu Arg Phe Gln Val Leu Glu Thr Ala Ser Tyr Asn Gly
 279 405 410 415
 282 Val Leu Ile Trp Lys Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala
 283 420 425 430
 286 Val Met Gly Lys Thr Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly
 287 435 440 445
 290 Tyr Phe Gly Tyr Lys Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly
 291 450 455 460
 294 Met Gly Lys Gly Thr His Leu Ser Leu Phe Phe Val Ile Met Arg Gly
 295 465 470 475 480
 298 Glu Tyr Asp Ala Leu Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu
 299 485 490 495
 302 Met Leu Met Asp Gln Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe
 303 500 505 510
 306 Lys Pro Asp Pro Asn Ser Ser Ser Phe Lys Lys Pro Thr Gly Glu Met
 307 515 520 525
 310 Asn Ile Ala Ser Gly Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu
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 314 Asn Gly Thr Tyr Ile Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val
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 318 Asp Thr Ser Asp Leu Pro Asp Pro
 319 565

322 <210> SEQ ID NO: 3

323 <211> LENGTH: 2359

324 <212> TYPE: DNA

325 <213> ORGANISM: Mouse Sp.

327 <400> SEQUENCE: 3

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 332 tcccttctga gtttctctag actccttaca gcgcacggca cagaatttca gtttcttaag 180
 334 atggagtcaa gcaaaaagat ggatgctgct ggcacactgc agcctaacc acccctaaag 240
 336 ctgcagcctg atcgcggcgc aggttcctg ctctgtccgg agcaaggagg ctacaaggag 300
 338 aagtttgtga agacgggtga agacaagtac aagtgcgaga agtgccgcct ggtgctgtgc 360
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 342 agctcctcca gtccaaaatg cacagcgtgc caagaaagca tcatcaaaga caaggtgttt 480
 344 aaggataatt gctgcaagag agagattctg gcccttcagg tctactgtcg gaatgaaggc 540
 346 agaggttgtg cggagcagct gactctggga catctgctgg tgcacctaaa aaatgaatgt 600
 348 cagtttgagg aacttccctg tctgcgtgcc gactgcaaag aaaaagtact gagaaaagac 660
 350 ttgcgggata acgtggaaaa ggcctgtaaa taccgcgagg ccacgtgcag tcaactgcaag 720
 352 agccaagtgc ccatgatcaa actgcagaaa catgaagaca cagattgtcc ctgtgtggtg 780
 354 gtatcctgcc ctcaaaagtg cagcgttcag actcttctaa ggagtgaagt gagtgcacac 840
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372 gagtcccagc tgagccggca tgaccagacg ttgagtgttc atgacatccg cttggccgac 1380
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378 agccagcctt tctacacagg ttatttttggc tataagatgt gtgccagggt ctacctgaat 1560
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382 tatgatgtc tgttgccatg gccgttcaag cagaaagtga cacttatgct gatggatcag 1680
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409 <210> SEQ ID NO: 4
410 <211> LENGTH: 2455
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412 <213> ORGANISM: Homo Sapiens
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VERIFICATION SUMMARY

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Output Set: N:\CRF3\06272002\H813323B.raw

L:13 M:270 C: Current Application Number differs, Wrong Format

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date